SA3

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: THE GENERAL HOSPITAL CORPORATION FRUIT STREET

BOSTON, MA 02114

UNITED STATES OF AMERICA

APPLICANT/INVENTOR: de la Monte, Suzanne Wands, Jack R.

- (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 - (B) STREET: 1100 New York Ave., Suite 600
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To be assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/038,908
 - (B) FILING DATE: 26-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Esmond, Robert W.
 - (B) REGISTRATION NUMBER: 32,893
 - (C) REFERENCE/DOCKET NUMBER: 0609.437PC01
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1442 base pairs

Applicant's or agent's file	•
reference number 0609.437PC01	

International	application
TDA	

aternational application	

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM (PCT Rule 13bis)

A									
A. The indications made below relate to the microorganism	m referred to in the description on page5_, line11								
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet								
Name of depositary institution AMERICAN TYPE CULTURE COLLECTION									
Address of depositary institution (including postal code and cour	ntry)								
12301 Parklawn Drive Rockville, Maryland 20852 United States of America									
Date of deposit March 16, 1993	Accession Number 69262								
C. ADDITIONAL INDICATIONS (leave blank if not appl	licable) This information is continued on an additional sheet \Box								
Escherichia coli: AD10-7-DH1									
D. DESIGNATED STATES FOR WHICH INDICATION	ONS ARE MADE (if the indications are not for all designated States)								
n one in the second of the sec									
E. SEPARATE FURNISHING OF INDICATIONS (leave									
The indications listed below will be submitted to the international "Accession Number of Deposit")	Bureau later (specify the general nature of the indications, e.g.,								
	·								
•									
For receiving Office use only	For International Bureau use only								
☐ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:								
Authorized officer	Authorized officer								
J 1	,								

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 - (i) APPLICANT: de la Monte, Suzanne Wands, Jack R.
 - (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease
 - (iii) NUMBER OF SEQUENCES: 14
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 - (C) CITY: Washington
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 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
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 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Esmond, Robert W.
 - (B) REGISTRATION NUMBER: 32,893
 - (C) REFERENCE/DOCKET NUMBER: 0609.4370000
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 15..1139
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC

Met Glu Phe Ser Leu Leu Pro Arg Leu Glu Cys

1 10

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 15..1139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ттт	TTTT	TTT	TGAG	ATG Met	Glu	TTT Phe	TCG Ser	CTC Leu	ı Leı	TTC Let	CC0	C AGO Arg	G CTO J Let	ı Glı	TGC LCys		50
AAT Asn	Gly GGC	GCA Ala 15	Ile	TCA Ser	GCT Ala	CAC His	CGC Arg 20	Asn	CTC Leu	CGC Arg	CTC Leu	C CCG Pro 25	Gl3	TC/ Sei	A AGC	:	98
GAT Asp	TCT Ser 30	Pro	GCC Ala	TCA Ser	GCC Ala	TCC Ser 35	CCA Pro	GTA Val	GCT Ala	GGG	ATI Ile 40	Thr	GGC Gly	ATO Met	TGC Cys		146
ACC Thr 45	CAC His	GCT Ala	CGG Arg	CTA Leu	ATT Ile 50	TTG Leu	TAT Tyr	· TTT Phe	TTT Phe	TTA Leu 55	GTA Val	GAG Glu	ATG Met	GAG Glu	TTT Phe 60		194
CTC Leu	CAT His	GTT Val	GGT Gly	CAG Gln 65	GCT Ala	GGT Gly	CTC Leu	GAA Glu	CTC Leu 70	CCG Pro	ACC Thr	TCA Ser	GAT Asp	GAT Asp 75	CCC Pro		242
TCC Ser	GTC Val	TCG Ser	GCC Ala 80	TCC Ser	CAA Gln	AGT Ser	GCT Ala	AGA Arg 85	TAC Tyr	AGG Arg	ACT	GGC Gly	CAC His 90	CAT His	GCC Ala		290
CGG Arg	CTC Leu	TGC Cys 95	CTG Leu	GCT Ala	AAT Asn	TTT Phe	TGT Cys 100	GGT Gly	AGA Arg	AAC Asn	AGG Arg	GTT Val 105	TCA Ser	CTG Leu	ATG Met		338
TGC Cys	CCA Pro 110	AGC Ser	TGG Trp	TCT Ser	CCT Pro	GAG Glu 115	CTC Leu	AAG Lys	CAG Gln	TCC Ser	ACC Thr 120	TGC Cys	CTC Leu	AGC Ser	CTC Leu		.386
CCA Pro 125	AAG Lys	TGC Cys	TGG Trp	GAT Asp	TAC Tyr 130	AGG Arg	CGT Arg	GCA Ala	GCC Ala	GTG Val 135	CCT Pro	GGC Gly	CTT Leu	TTT Phe	ATT Ile 140		434
TTA Leu	TTT Phe	TTT Phe	TTA Leu	AGA Arg 145	CAC His	AGG Arg	TGT Cys	CCC Pro	ACT Thr 150	CTT Leu	ACC Thr	CAG Gln	GAT Asp	GAA Glu 155	GTG Val		482
CAG Gln	TGG Trp	TGT Cys	GAT Asp	CAC His	AGC Ser	TCA Ser	CTG Leu	CAG Gln	CCT Pro	TCA Ser	ACT Thr	CCT Pro	GAG Glu	ATC Ile	AAG Lys		530

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			16	o				16	5				17	0		
CA'	T CC' s Pro	F CC Pr 17	o Ala	C TC/	A GCC	C TCC	C CA. Gl: 180	n Va	A GC 1 Al	T GG a Gl	G AC y Th	C AA r Ly 18	s As	C AT p Me	G CAC t His	578
CA(TAC Tyl 190	Th:	C TGO	G CTA	A ATT	TTT Phe 195	: Ile	r TT' ∋ Phe	r At e Il	T TT	T AA e As 20	n Phe	T TT	G AG	A CAG g Gln	626
AGT Ser 205	: Lei	AA(Asr	C TCT	GTC Val	ACC Thr 210	Gln	GCT Ala	r GGA a Gly	A GTO	G CAG L Gli 215	n Trp	G CGO	C AA' J Asi	r CT'	GGC Gly 220	674
TC <i>P</i> Ser	CTC Leu	CA# Glr	A CCT	CTG Leu 225	Pro	CCC Pro	GGC	TTC Phe	230	Let	A TT(i Ph∈	C TCC Ser	TGC Cys	C CCC Fro 235	AGC Ser	722
CTC Leu	CTG Leu	AGT Ser	AGC Ser 240	Trp	GAC Asp	TAC Tyr	AGG Arg	CGC Arg 245	Pro	A CCA Pro	A CGC Arg	CTA Leu	GCT Ala 250	Asn	TTT Phe	770
TTT Phe	GTA Val	TTT Phe 255	Leu	GTA Val	GAG Glu	ATG Met	GGG Gly 260	Phe	ACC Thr	ATG Met	TTC Phe	GCC Ala 265	AGG Arg	TTG Leu	ATC Ile	818
TTG Leu	ATC Ile 270	TCT Ser	GGA Gly	CCT Pro	TGT Cys	GAT Asp 275	CTG Leu	CCT Pro	GCC Ala	TCG Ser	GCC Ala 280	TCC Ser	CAA Gln	AGT Ser	GCT Ala	866
GGG Gly 285	ATT	ACA Thr	GGC Gly	GTG Val	AGC Ser 290	CAC His	CAC His	GCC Ala	CGG Arg	CTT Leu 295	ATT Ile	TTT Phe	AAT Asn	TTT Phe	TGT Cys 300	914
TTG Leu	TTT Phe	GAA Glu	ATG Met	GAA Glu 305	TCT Ser	CAC His	TCT Ser	GTT Val	ACC Thr 310	CAG Gln	GCT Ala	GGA Gly	GTG Val	CAA Gln 315	TGG Trp	962
CCA Pro	AAT Asn	Leu	GGC Gly 320	TCA Ser	CTG Leu	CAA Gln	CCT Pro	CTG Leu 325	CCT Pro	CCC Pro	GGG Gly	CTC Leu	AAG Lys 330	CGA Arg	TTC Phe	1010
TCC Ser	TGT Cys	CTC Leu 335	AGC Ser	CTC Leu	CCA Pro	AGC Ser	AGC Ser 340	TGG Trp	GAT Asp	TAC Tyr	GGG Gly	CAC His 345	CTG Leu	CCA Pro	CCA Pro	1058
CAC His	CCC Pro 350	GCT Ala	AAT Asn	TTT Phe	TGT Cys	ATT Ile 355	TTC Phe	ATT Ile	AGA Arg	GGC Gly	GGG Gly 360	GTT Val	TCA Ser	CCA Pro	TAT Tyr	1106
TTG Leu 365	TCA Ser	GGC Gly	TGG Trp	Ser	CAA Gln 370	ACT Thr	CCT Pro	GAC Asp	CTC Leu	AGG Arg 375	TGAC	CCAC	CT G	ССТС	AGCCT	1159

TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA

1219

AAATATGTAG	CAATGGGGG	TCTTGCTATG	TTGCCCAGGC	TGGTCTCAAA	CTTCTGGCTT	1279
CATGCAATCC	TTCCAAATGA	GCCACAACAC	CCAGCCAGTC	ACATTTTTA	AACAGTTACA	1339
TCTTTATTTT	AGTATACTAG	AAAGTAATAC	AATAAACATG	TCAAACCTGC	AAATTCAGTA	1399
GTAACAGAGT	TCTTTTATAA	CTTTTAAACA	AAGCTTTAGA	GCA		1442

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:.
- Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile 1 5 10 15
- Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala 20 25 30
- Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg 35 40 45
- Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
 50 55 60
- Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala 65 70 75 80
- Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu 85 90 95
- Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
 100 105 110
- Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp 115 120 125
- Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu 130 135 140
- Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp 145 150 155 160
- His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala 165 170 175
- Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp 180 185 190

Leu	Ile	Phe 195	e Il∈	Phe	e Ile	Ph∈	200	Phe	e Leu	a Arg	Gln	Ser 205		a Asr	Ser
Val	Thr 210	Gln	Ala	Gly	v Val	Gln 215	Trp	Arg	Asn	Leu	Gly 220	Ser	Leu	Gln	Pro
Leu 225	Pro	Pro	Gly	Phe	Lys 230	Leu	Phe	Ser	Cys	Pro 235	Ser	Leu	Leu	Ser	Ser 240
Trp	Asp	Tyr	Arg	Arg 245	Pro	Pro	Arg	Leu	Ala 250	Asn	Phe	Phe	Val	Phe 255	Leu
Val	Glu	Met	Gly 260	Phe	Thr	Met	Phe	Ala 265	Arg	Leu	Ile	Leu	Ile 270	Ser	Gly
Pro	Cys	Asp 275	Leu	Pro	Ala	Ser	Ala 280	Ser	Gln	Ser	Ala	Gly 285	Ile	Thr	Gly
Val	Ser 290	His	His	Ala	Arg	Leu 295	Ile	Phe	Asn	Phe	C y s 300-	Leu	Phe	Glu	Met
Glu 305	Ser	His	Ser	Val	Thr 310	Gln	Ala	Gly	Val	Gln 315	Trp	Pro	Asn	Leu	Gly 320
Ser	Leu	Gln	Pro	Leu 325	Pro	Pro	Gly	Leu	Lys 330	Arg	Phe .	Ser		Leu 335	Ser
Leu	Pro	Ser	Ser 340	Trp	Asp	Tyr	Gly	His 345	Leu	Pro	Pro I		Pro . 350	Ala	Asn
Phe (Cys	Ile 355	Phe	Ile	Arg	Gly	Gly 360	Val	Ser	Pro !		Leu : 365	Ser (Gly	Trp
Ser (Gln ' 370	Thr :	Pro .	Asp	Leu i	Arg 375									
(2)	NFO	RMAT	ION	FOR :	SEQ :	ID NO	0:3:								
	(i)	SEQUAL (A)	LE	1GTH	ARACT	31 ba	ase p	S: pairs	5						

- (C) STRANDEDNESS: double (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTT	GAGATGGAGT	TTTCGCTCTT	GTTGCCCAGG	CTGGAGTGCA	ATGGCGCAAT	60
CTCAGCTCAC	CGCAACCTCC	GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	120
AGTAGCTGGG	ATTACAGGCA	TGTGCACCAC	GCTCGGCTAA	TTTTGTATTT	TTTTTTAGTA	180

GAGATGGAGT	TTAACTCCAT	GTTGGTCAGG	CTGGTCTCG#	ACTCCCGAC	TCAGATGATC	240
TCCCGTCTCG	GCCTGCCCAA	AGTGCTGAGA	TTACAGGCAT	GAGCCACCAT	GCCCGGCCTC	300
TGCCTGGCTA	ATTTTTGTGG	TAGAAACAGG	GTTTCACTGA	TGTTGCCCA	GCTGGTCTCC	360
TGAGCTCAAG	CAGTCCACCT	GCCTCAGCCT	CCCAAAGTGC	TGGGATTACA	GGCGTCAGCC	420
GTGCCTGGCC	TTTTTATTT	ATTTTTTTA	AGACACAGGT	GTACCACTCT	TACCCAGGAT	480
GAAGTGCAGT	GGTGTGATCA	CAGCTCACTG	CAGCCTTCAA	CTCCTGAGAT	CAAGCAATCC	540
TCCTGCCTCA	GCCTCCCAAG	TAGCTGGGAC	CAAAGACATG	CACCACTACA	CCTGGTAATT	600
TTTATTTTA	TTTTTAATTT	TTTGAGACAG	AGTCTCACTC	TGTCACCCAG	GCTGGAGTGC	660
AGTGGCGCAA	TCTTGGCTCA	CTGCAACCTC	TGCCTCCCGG	GTTCAAGTTA	TTCTCCTGCC	720
CCAGCCTCCT	GAGTAGCTGG	GACTACAGGC	GCCCACCACG	CCTAGCTAAT	TTTTTTGTAT	780
TTTTAGTAGA	GATGGGGTTT	CACCATGTTC	GCCAGGTTGA	TCTTGATCTC	TTGACCTTGT	840
GATCTGCCTG	CCTCGGCCTA	CCCAAAGTGC	TGGGATTACA	GGTCGTGACT	CCACGCCGGC	900
CTATTTTTAA	TTTTTGTTTG	TTTGAAATGG	AATCTCACTC	TGTTACCCAG	GTCGGAGTGC	960
AATGGCAAAT	CTCGGCTACT	CGCAACCTCT	GCCTCCCGGG	TCAAGCGATT	CTCCTGTCTC	1020
AGCCTCCCAA	GCAGCTGGGA	TTACGGGACC	TGCACCACAC	CCCGCTAATT	TTTGTATTTT	1080
CATTAGAGGC	GGGTTTACCA	TATTTGTCAG	GCTGGGTCTC	AAACTCCTGA	CCTCAGGTGA	1140
CCACCTGCC	TCAGCCTTCC	AAAGTGCTGG	GATTACAGGC	GTGAGCCACC	TCACCCAGCC	1200
GCTAATTTG	GAATAAAAAA	TATGTAGCAA	TGGGGGTCTG	CTATGTTGCC	CAGGCTGGTC	1260
CAAACTTCT	GGCTTCAGTC	AATCCTTCCA	AATGAGCCAC	AACACCCAGC	CAGTCACATT	1320
TTTAAACAG	TTACATCTTT	ATTTTAGTAT	ACTAGAAAGT	ААТАСААТАА	ACATGTCAAA	1380
						1381

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTT	' GAGATGGAGT	TTTCGCTCTT	GTTGCCCAGG	G CTGGAGTGC	A ATGGCGCAAT	60
CTCAGCTCAC	CGCAACCTCC	GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	120
AGTAGGCTGG	GATTACAGGC	ATGTGCACCA	CGCTCGGCTA	ATTTTGTAT	TTTTTTTAGT	180
AGAGATGGAG	TTTCTCCATG	TTGGTCAGGC	TGGTCTCGAA	CTCCGACCTC	AGATGATCCT	240
CCCGTCTCGG	CCTCCCAAAG	TGCTAGATAC	AGGACTGAGC	ACCATGCCCG	GCCTCTGCCT	300
GGCTAATTTT	TGTGGTAGAA	ACAGGGTTTC	ACTGATGTGC	CCAAGCTGGT	CTCCTGAGCT	360
CAAGCAGTCC	ACCTGCCTCA	GCCTCCCAAA	GTGCTGGGAT	TACAGGCGTG	CAGCCGTGCC	420
TGGCCTTTTT	ATTTTATTTT	TTTTAAGACA	CAGGTGTCCC	ACTCTTACCC	AGGATGAAGT	480
GCAGTGGTGT	GATCACAGCT	CACTGCAGCC	TTCAACTCTG	AGATCAAGCA	TCCTCCTGCC	540
TCAGCCTCCC	AAAGTAGCTG	GGACCAAAGA	CATGCACCAC	TACACCTGGC	TAATTTTTAT	600
TTTTATTTT	AATTTTTTGA	GACAGAGTCT	CAACTCTGTC	ACCCAGGCTG	GAGTGCAGTG	660
GCGCAATCTT	GGCTCACTGC	AACCTCTGCC	TCCCGGGTTC	AAGTTATTCT	CCTGCCCCAG	720
CCTCCTGAGT	AGCTGGGACT	ACAGGCGCCC	ACCACGCCTA	GCTAATTTT	TTGTATTTT	780
AGTAGAGATG	GGGTTTCACC	ATGTTCGCCA	GGTTGATGCT	AGATCTCTTG	ACCTTGTGAT	840
CTGCCTGCCT	CGGCCTCCCA	AAGTGCTGGG	ATTACAGGAC	GTGACGCCCA	CCGCCCGGCC	900
TATTTTTAAT	TTTTGTTTGT	TTGAAATGGA	ATCTCACTCT	GTTACCCAGG	CTGGAGTGCA	960
ATGGCCAAAT	CTCGGCTCAC	TGCAACCTCT	GCCTCCCGGG	CTCAAGCGAT	TCTCCTGTCT	1020
CAGCCTCCCA	AGCAGCTGGG	ATTACGGGCA	CCTGCACCAC	ACCCCGCTAA	TTTTTGTATT	1080
TTCATTAGAG	GCGGGGTTTC	ACCATATTTG	TCAGGCTGGT	CTCAAACTCC	TGACCTCAGG	1140
TGACCCACCT	GCCTCAGCCT	TCCAAAGTGC	TGGGATTACA	GGCGTGACGC	CTCACCCAGC	1200
CGGCTAATTT	AGATAAAAA	ATATGTAGCA	ATGGGGGGTC	TTGCTATGTT	GCCCAGGCTG	1260
GTCTCAAACT	TCTGGCTTCA	TGCAATCCTT	CCAAATGAGC	CACAACACCC	AGCCAGTCAC	1320
ATTTTTAAAC	AGTTACATCT	TTATTTTAGT	ATACTAGAAA	GTGATACGAT	AACATGGCGG	1380
AACCTGCAAA	TTCGAGTAGT	ACAGAGTCTT	TTATAACT			1418

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
TGTCCCACTC TTACCCAGGA TG	2
(2) INFORMATION FOR SEQ ID NO:6:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
•	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
AAGCAGGCAG ATCACAAGGT CCAG	24
(2) INFORMATION FOR SEQ ID NO:7:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
AATGGATGAC GATATCGCTG	20
(2) INFORMATION FOR SEQ ID NO:8:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 19 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:		
ATGAGGTAGT CTGTCAGGT		19
(2) INFORMATION FOR SEQ ID NO:9:		
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:		
TTCATCCTGG GTAAGAGTGG GACACCTGTG		30
(2) INFORMATION FOR SEQ ID NO:10:		
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 26 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:		
TGGTGCATGT CTTTGGTCCC AGCTAC		26
(2) INFORMATION FOR SEQ ID NO:11:		
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 		
(ii) MOLECULE TYPE: cDNA		
	,	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	-	
ATCAACCTGG CGAACATGGT GAACCCCATC		30
(2) INFORMATION FOR SEQ ID NO:12:		

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE (C) STRAI	TH: 14 base pairs : nucleic acid NDEDNESS: single LOGY: linear	
(ii) MOLECULE 1	TYPE: cDNA	
•	•	
(xi) SEQUENCE [DESCRIPTION: SEQ ID NO:12	:
CACTGCACTT NCCA		14
(2) INFORMATION FOR	SEQ ID NO:13:	
(A) LENGT (B) TYPE: (C) STRAN	CHARACTERISTICS: CH: 14 base pairs nucleic acid DEDNESS: single OGY: linear	
(ii) MOLECULE T	YPE: cDNA	
\		
(xi) SEQUENCE D	ESCRIPTION: SEQ ID NO:13:	
CCAGGTGTAG NCCA		14
(2) INFORMATION FOR	SEQ ID NO:14:	
(A) LENGTI (B) TYPE: (C) STRANI	HARACTERISTICS: H: 14 base pairs nucleic acid DEDNESS: single DGY: linear	
(ii) MOLECULE TY	YPE: cDNA	
(xi) SEQUENCE DE	ESCRIPTION: SEQ ID NO:14:	
CAAGGTCCAG NCCA		14

					GCT Ala											98
					GCC Ala											146
					ATT Ile 50											194
					GCT Ala											242
					CAA Gln											290
					AAT Asn											338
					CCT Pro											386
					TAC Tyr 130											434
					CAC His											482
					AGC Ser											530
					GCC Ala											578
					ATT Ile											626
					ACC Thr 210											674
					CCT Pro											722
					GAC Asp											770
					GAG Glu											818
TTG	ATC	TCT	GGA	ССТ	TGT	GAT	CTG	CCT	GCC	TCG	GCC	TCC	CAA	AGT	GCT	866

Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe 320 TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro 335 CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr 350 TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg 375 TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTA AACAGTTACA TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA															
Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys 300 TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp 315 CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe 320 TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro 335 CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr 350 TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg 375 TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTA AACAGTTACA TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	Gln Ser Ala	er Gln			Ser	Ala	Pro	Leu	_	Cys	Pro	Gly	Ser		Leu
Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp 315 CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe 320 TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro 345 CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr 350 TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg 370 TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT CATGCAATCC TTCCAAATGA GCCACAACAC CCAGGCCAGTC ACATTTTTTA AACAGTTACA TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	Asn Phe Cys				Leu					Ser					Gly
Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe 320 TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro 335 CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr 350 TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg 375 TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTA AACAGTTACA TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	Val Gln Trp					Thr					Glu				
Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro 345 CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr 350 TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg 365 TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTA AACAGTTACA TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	Lys Arg Phe	eu Lys					Leu				Ser	Gly			
His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr 350 355 360 TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg 365 370 375 TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTA AACAGTTACA TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	Leu Pro Pro	is Leu	/ His					Ser					Leu		
Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg 365 370 375 TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTA AACAGTTACA TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA			/ Val	Gly					Ile					Pro	
AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTA AACAGTTACA TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	CCT GCCTCAGCCT 1159	CACCT (ACCCA	TGA	Arg					Gln					Leu
CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTA AACAGTTACA TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	AAT TTAGATAAAA 1219	CTAAT T	GGCT.	GCC	CCCA	CTCAC	ACC	BAGC	GCGT	CA G	ATTA	rgggz	rgc 1	AAAG	TCC
TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	AAA CTTCTGGCTT 1279	TCAAA (TCTC.	TGG	AGGC	GCCC	TTC	CTATO	CTTG	GG T	GGGG	CAATO	rag (ratg:	AAA
	TTA AACAGTTACA 1339	TTTTA A	ATTTT	ACA!	AGTC	AGCC	CCZ	AACA	CCAC	GA G	YAAA	rtcc	rcc 1	GCAAT	CAT
GTAACAGAGT TCTTTTATAA CTTTTAAACA AAGCTTTAGA GCA	TGC AAATTCAGTA 1399	CCTGC A	AACC	TCA	CATG	DAAAT	AA!	ATA	AAGT	AG A	ract:	AGTA	rtt A	TATT	TCT
	1442		7	GCA	raga	GCTT'	AA A	AAAC	r TTT 2	AA C'	TAT	CTT	AGT T	ACAGA	GTAZ

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile 1 5 10 15

Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala 20 25 30

Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
35 40 45

Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly 50 60

Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala 65 70 75 80

Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu

85 90 95

Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp 105 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu 135 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp 150 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala 170 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser 225 230 235 Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu 250 Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met 295 Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn 340 345 350 Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg

370 asp Leu arg

- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTT	GAGATGGAGT	TTTCGCTCTT	GTTGCCCAGG	CTGGAGTGCA	ATGGCGCAAT	60
CTCAGCTCAC	CGCAACCTCC	GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	120
AGTAGCTGGG	ATTACAGGCA	TGTGCACCAC	GCTCGGCTAA	TTTTGTATTT	TTTTTTAGTA	180
GAGATGGAGT	TTAACTCCAT	GTTGGTCAGG	CTGGTCTCGA	ACTCCCGACC	TCAGATGATC	240
TCCCGTCTCG	GCCTGCCCAA	AGTGCTGAGA	TTACAGGCAT	GAGCCACCAT	GCCCGGCCTC	300
TGCCTGGCTA	ATTTTTGTGG	TAGAAACAGG	GTTTCACTGA	TGTTGCCCAA	GCTGGTCTCC	360
TGAGCTCAAG	CAGTCCACCT	GCCTCAGCCT	CCCAAAGTGC	TGGGATTACA	GGCGTCAGCC	420
GTGCCTGGCC	TTTTTATTTT	ATTTTTTTA	AGACACAGGT	GTACCACTCT	TACCCAGGAT	480
GAAGTGCAGT	GGTGTGATCA	CAGCTCACTG	CAGCCTTCAA	CTCCTGAGAT	CAAGCAATCC	540
TCCTGCCTCA	GCCTCCCAAG	TAGCTGGGAC	CAAAGACATG	CACCACTACA	CCTGGTAATT	600
TTTATTTTTA	TTTTTAATTT	TTTGAGACAG	AGTCTCACTC	TGTCACCCAG	GCTGGAGTGC	660
AGTGGCGCAA	TCTTGGCTCA	CTGCAACCTC	TGCCTCCCGG	GTTCAAGTTA	TTCTCCTGCC	720
CCAGCCTCCT	GAGTAGCTGG	GACTACAGGC	GCCCACCACG	CCTAGCTAAT	TTTTTTGTAT	780
TTTTAGTAGA	GATGGGGTTT	CACCATGTTC	GCCAGGTTGA	TCTTGATCTC	TTGACCTTGT	840
GATCTGCCTG	CCTCGGCCTA	CCCAAAGTGC	TGGGATTACA	GGTCGTGACT	CCACGCCGGC	900
СТАТТТТТАА	TTTTTGTTTG	TTTGAAATGG	AATCTCACTC	TGTTACCCAG	GTCGGAGTGC	960
AATGGCAAAT	CTCGGCTACT	CGCAACCTCT	GCCTCCCGGG	TCAAGCGATT	CTCCTGTCTC	1020
AGCCTCCCAA	GCAGCTGGGA	TTACGGGACC	TGCACCACAC	CCCGCTAATT	TTTGTATTTT	1080
CATTAGAGGC	GGGTTTACCA	TATTTGTCAG	GCTGGGTCTC	AAACTCCTGA	CCTCAGGTGA	1140
CCCACCTGCC	TCAGCCTTCC	AAAGTGCTGG	GATTACAGGC	GTGAGCCACC	TCACCCAGCC	1200
GGCTAATTTG	GAATAAAAAA	TATGTAGCAA	TGGGGGTCTG	CTATGTTGCC	CAGGCTGGTC	1260
TCAAACTTCT	GGCTTCAGTC	AATCCTTCCA	AATGAGCCAC	AACACCCAGC	CAGTCACATT	1320
TTTTAAACAG	TTACATCTTT	ATTTTAGTAT	ACTAGAAAGT	AATACAATAA	ACATGTCAAA	1380
С						1381

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA



TTTTTTTTT	GAGATGGAGT	TTTCGCTCTT	GTTGCCCAGG	CTGGAGTGCA	ATGGCGCAAT	60
CTCAGCTCAC	CGCAACCTCC	GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	120
AGTAGGCTGG	GATTACAGGC	ATGTGCACCA	CGCTCGGCTA	ATTTTGTATT	TTTTTTTAGT	180
AGAGATGGAG	TTTCTCCATG	TTGGTCAGGC	TGGTCTCGAA	CTCCGACCTC	AGATGATCCT	240
CCCGTCTCGG	CCTCCCAAAG	TGCTAGATAC	AGGACTGAGC	ACCATGCCCG	GCCTCTGCCT	300
GGCTAATTTT	TGTGGTAGAA	ACAGGGTTTC	ACTGATGTGC	CCAAGCTGGT	CTCCTGAGCT	360
CAAGCAGTCC	ACCTGCCTCA	GCCTCCCAAA	GTGCTGGGAT	TACAGGCGTG	CAGCCGTGCC	420
TGGCCTTTTT	ATTTTATTT	TTTTAAGACA	CAGGTGTCCC	ACTCTTACCC	AGGATGAAGT	480
GCAGTGGTGT	GATCACAGCT	CACTGCAGCC	TTCAACTCTG	AGATCAAGCA	TCCTCCTGCC	540
TCAGCCTCCC	AAAGTAGCTG	GGACCAAAGA	CATGCACCAC	TACACCTGGC	TAATTTTTAT	600
TTTTATTTT	AATTTTTTGA	GACAGAGTCT	CAACTCTGTC	ACCCAGGCTG	GAGTGCAGTG	660
GCGCAATCTT	GGCTCACTGC	AACCTCTGCC-	TCCCGGGTTC	AAGTTATTCT	CCTGCCCCAG	720
CCTCCTGAGT	AGCTGGGACT	ACAGGCGCCC	ACCACGCCTA	GCTAATTTTT	TTGTATTTTT	780
AGTAGAGATG	GGGTTTCACC	ATGTTCGCCA	GGTTGATGCT	AGATCTCTTG	ACCTTGTGAT	840
CTGCCTGCCT	CGGCCTCCCA	AAGTGCTGGG	ATTACAGGAC	GTGACGCCCA	CCGCCCGGCC	900
TATTTTTAAT	TTTTGTTTGT	TTGAAATGGA	ATCTCACTCT	GTTACCCAGG	CTGGAGTGCA	960
ATGGCCAAAT	CTCGGCTCAC	TGCAACCTCT	GCCTCCCGGG	CTCAAGCGAT	TCTCCTGTCT	1020
CAGCCTCCCA	AGCAGCTGGG	ATTACGGGCA	CCTGCACCAC	ACCCCGCTAA	TTTTTGTATT	1080
TTCATTAGAG	GCGGGGTTTC	ACCATATTTG	TCAGGCTGGT	CTCAAACTCC	TGACCTCAGG	1140
TGACCCACCT	GCCTCAGCCT	TCCAAAGTGC	TGGGATTACA	GGCGTGACGC	CTCACCCAGC	1200
CGGCTAATTT	AGATAAAAAA	ATATGTAGCA	ATGGGGGGTC	TTGCTATGTT	GCCCAGGCTG	1260
GTCTCAAACT	TCTGGCTTCA	TGCAATCCTT	CCAAATGAGC	CACAACACCC	AGCCAGTCAC	1320
ATTTTTAAAC	AGTTACATCT	TTATTTTAGT	ATACTAGAAA	GTGATACGAT	AACATGGCGG	1380
AACCTGCAAA	TTCGAGTAGT	ACAGAGTCTT	ТТАТААСТ			1418

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

(2) INFORMATION FOR SEQ ID NO:9:

(ii) MOLECULE TYPE: cDNA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:9:	
TTCATCCT	GG GTAAGAGTGG GACACCTGTG	30
(2) INFO	RMATION FOR SEQ ID NO:10:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:10:	
TGGTGCAT	GT CTTTGGTCCC AGCTAC	26
(2) INFO	RMATION FOR SEQ ID NO:11:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:11:	
ATCAACCT	GG CGAACATGGT GAACCCCATC	30
(2) INFO	RMATION FOR SEQ ID NO:12:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:12:	
CACTGCAC'	TT NCCA	14
(2) INFO	RMATION FOR SEQ ID NO:13:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
CCAGGTGTAG NCCA	14
(2) INFORMATION FOR SEQ ID NO:14:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
CAAGGTCCAG NCCA	14